

# Comprehensive comparative analysis of 5'€²-end RNA-

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Citation Report

#	ARTICLE	IF	CITATIONS
1	SLIC-CAGE: high-resolution transcription start site mapping using nanogram-levels of total RNA. <i>Genome Research</i> , 2018, 28, 1943-1956.	2.4	33
2	Rhythms of the Genome: Circadian Dynamics from Chromatin Topology, Tissue-Specific Gene Expression, to Behavior. <i>Trends in Genetics</i> , 2018, 34, 915-926.	2.9	43
3	Maximizing the Utility of Cancer Transcriptomic Data. <i>Trends in Cancer</i> , 2018, 4, 823-837.	3.8	32
4	NanoPARE: parallel analysis of RNA 5' ends from low-input RNA. <i>Genome Research</i> , 2018, 28, 1931-1942.	2.4	56
5	Perspectives on topology of the human m <sup>1</sup> A methylome at single nucleotide resolution. <i>Rna</i> , 2018, 24, 1437-1442.	1.6	19
6	RNA sequencing: the teenage years. <i>Nature Reviews Genetics</i> , 2019, 20, 631-656.	7.7	1,192
7	Computational Biology Solutions to Identify Enhancers-target Gene Pairs. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 821-831.	1.9	29
8	MAPCap allows high-resolution detection and differential expression analysis of transcription start sites. <i>Nature Communications</i> , 2019, 10, 3219.	5.8	16
9	CAGEfightR: analysis of 5'-end data using R/Bioconductor. <i>BMC Bioinformatics</i> , 2019, 20, 487.	1.2	59
10	FFPEcap-seq: a method for sequencing capped RNAs in formalin-fixed paraffin-embedded samples. <i>Genome Research</i> , 2019, 29, 1826-1835.	2.4	9
11	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , 2019, 51, 1369-1379.	9.4	72
12	Comprehensive profiling of the fission yeast transcription start site activity during stress and media response. <i>Nucleic Acids Research</i> , 2019, 47, 1671-1691.	6.5	34
13	Computation Resources for Molecular Biology: Special Issue 2019. <i>Journal of Molecular Biology</i> , 2019, 431, 2395-2397.	2.0	0
14	The landscape of transcription initiation across latent and lytic KSHV genomes. <i>PLoS Pathogens</i> , 2019, 15, e1007852.	2.1	13
15	Improved annotation of the domestic pig genome through integration of Iso-Seq and RNA-seq data. <i>BMC Genomics</i> , 2019, 20, 344.	1.2	80
16	Evidence that alternative transcriptional initiation is largely nonadaptive. <i>PLoS Biology</i> , 2019, 17, e3000197.	2.6	46
17	Discovery of gene regulatory elements through a new bioinformatics analysis of haploid genetic screens. <i>PLoS ONE</i> , 2019, 14, e0198463.	1.1	0
18	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , 2019, 47, D752-D758.	6.5	172

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19	<i>Saccharomyces cerevisiae</i> displays a stable transcription start site landscape in multiple conditions. <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	10
20	Different Plant Species Have Common Sequence Features Related to mRNA Degradation Intermediates. <i>Plant and Cell Physiology</i> , 2020, 61, 53-63.	1.5	8
21	High resolution biosensor to test the capping level and integrity of mRNAs. <i>Nucleic Acids Research</i> , 2020, 48, e129-e129.	6.5	8
22	Embryonic tissue differentiation is characterized by transitions in cell cycle dynamic-associated core promoter regulation. <i>Nucleic Acids Research</i> , 2020, 48, 8374-8392.	6.5	8
23	Simple and efficient profiling of transcription initiation and transcript levels with STRIPE-seq. <i>Genome Research</i> , 2020, 30, 910-923.	2.4	23
24	The Rubber Tree Genome. <i>Compendium of Plant Genomes</i> , 2020, , .	0.3	3
25	Optimized design of antisense oligomers for targeted rRNA depletion. <i>Nucleic Acids Research</i> , 2021, 49, e5-e5.	6.5	11
26	Changes in mRNA Degradation Efficiencies under Varying Conditions Are Regulated by Multiple Determinants in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2021, 62, 143-155.	1.5	2
27	The origin and evolution of a distinct mechanism of transcription initiation in yeasts. <i>Genome Research</i> , 2021, 31, 51-63.	2.4	18
28	High-Resolution Mapping of Transcription Initiation in the Asexual Stages of <i>Toxoplasma gondii</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 617998.	1.8	11
30	Cross-species RNA-seq for deciphering host-microbe interactions. <i>Nature Reviews Genetics</i> , 2021, 22, 361-378.	7.7	52
31	Transcription initiation mapping in 31 bovine tissues reveals complex promoter activity, pervasive transcription, and tissue-specific promoter usage. <i>Genome Research</i> , 2021, 31, 732-744.	2.4	11
34	FINDER: an automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences. <i>BMC Bioinformatics</i> , 2021, 22, 205.	1.2	17
35	Altered visual processing in the mdx52 mouse model of Duchenne muscular dystrophy. <i>Neurobiology of Disease</i> , 2021, 152, 105288.	2.1	4
36	High-quality reference genome for <i>Clonorchis sinensis</i> . <i>Genomics</i> , 2021, 113, 1605-1615.	1.3	19
38	TERA-Seq: true end-to-end sequencing of native RNA molecules for transcriptome characterization. <i>Nucleic Acids Research</i> , 2021, 49, e115-e115.	6.5	18
39	Identifying transcript 5' capped ends in <i>Plasmodium falciparum</i> . <i>PeerJ</i> , 2021, 9, e11983.	0.9	2
40	Current and Future Perspectives of Noncoding RNAs in Brain Function and Neuropsychiatric Disease. <i>Biological Psychiatry</i> , 2022, 91, 183-193.	0.7	15

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41	Cap analysis of gene expression (CAGE) and noncoding regulatory elements. <i>Seminars in Immunopathology</i> , 2022, 44, 127-136.	2.8	3
42	Global approaches for profiling transcription initiation. <i>Cell Reports Methods</i> , 2021, 1, 100081.	1.4	11
46	A step-by-step guide to analyzing CAGE data using R/Bioconductor. <i>F1000Research</i> , 2019, 8, 886.	0.8	23
47	Clinical and Translational Research Challenges in Neuroendocrine Tumours. <i>Current Medicinal Chemistry</i> , 2020, 27, 4823-4839.	1.2	5
54	Construction of Metatranscriptomic Libraries for 5â€™ End Sequencing of rRNAs for Microbiome Research. <i>Methods in Molecular Biology</i> , 2022, 2349, 137-146.	0.4	1
56	Genome-Wide Analysis of Transcription Start Sites and Core Promoter Elements in <i>Hevea brasiliensis</i> . <i>Compendium of Plant Genomes</i> , 2020, , 81-91.	0.3	0
57	Identification of high-confidence human poly(A) RNA isoform scaffolds using nanopore sequencing. <i>Rna</i> , 2022, 28, 162-176.	1.6	12
58	Spontaneous pulmonary emphysema in mice lacking all three nitric oxide synthase isoforms. <i>Scientific Reports</i> , 2021, 11, 22088.	1.6	3
59	Comprehensive determination of transcription start sites derived from all RNA polymerases using ReCappable-seq. <i>Genome Research</i> , 2022, 32, 162-174.	2.4	14
62	TSS-seq of <i>Toxoplasma gondii</i> sporozoites revealed a novel motif in stage-specific promoters. <i>Infection, Genetics and Evolution</i> , 2022, 98, 105213.	1.0	1
63	A comparison of experimental assays and analytical methods for genome-wide identification of active enhancers. <i>Nature Biotechnology</i> , 2022, 40, 1056-1065.	9.4	28
64	Nanopore ReCappable sequencing maps SARS-CoV-2 5â€™ capping sites and provides new insights into the structure of sgRNAs. <i>Nucleic Acids Research</i> , 2022, 50, 3475-3489.	6.5	12
66	Methods for detecting RNA degradation intermediates in plants. <i>Plant Science</i> , 2022, 318, 111241.	1.7	3
67	Exogenous artificial DNA forms chromatin structure with active transcription in yeast. <i>Science China Life Sciences</i> , 2021, , 1.	2.3	15
68	&lt;i>TP53BP1</i>, a New Dual-Coding Gene, Uses Promoter Switching and Translational Reinitiation to Express a smORF Protein that Interacts With the Proteasome. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
69	Bookend: precise transcript reconstruction with end-guided assembly. <i>Genome Biology</i> , 2022, 23, .	3.8	5
72	SCAFE: a software suite for analysis of transcribed cis-regulatory elements in single cells. <i>Bioinformatics</i> , 2022, 38, 5126-5128.	1.8	6
73	Sequence features around cleavage sites are highly conserved among different species and a critical determinant for RNA cleavage position across eukaryotes. <i>Journal of Bioscience and Bioengineering</i> , 2022, 134, 450-461.	1.1	0

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74	Simple and accurate transcriptional start site identification using Smar2C2 and examination of conserved promoter features. <i>Plant Journal</i> , 2022, 112, 583-596.	2.8	8
75	FIPRESCI: droplet microfluidics based combinatorial indexing for massive-scale 5' end single-cell RNA sequencing. <i>Genome Biology</i> , 2023, 24, .	3.8	4
77	Sex-chromosome mechanisms in cardiac development and disease. , 2023, 2, 340-350.		1